RAW SEQUENCE LISTING
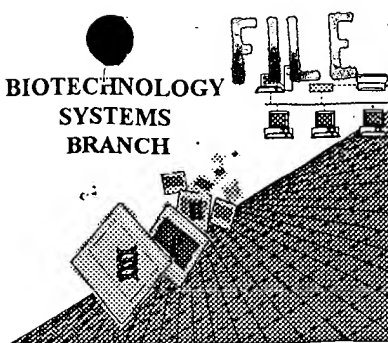# ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer-readable
form:

RECEIVED

Application Serial Number: _09/267,963__

APR 0 4 2001

TECH CENTER 1600/2900

Source: _1647_

Date Processed by STIC: _3/27/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE**
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A**
   NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program
employing a logical and intuitive user-interface to check whether a sequence listing is in
compliance with format and content rules. Checker Version 3.0 works for sequence listings
generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old
rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual
Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-
compliant. Checker allows public users to check sequence listings in Computer Readable form
(CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence
listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED   SUGGESTED   CORRECTION

SERIAL NUMBER: _09/267,963β_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ **Wrapped Nucleics**
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ **Wrapped Aminos**
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ **Incorrect Line Length**
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 ✓ **Misaligned Amino Acid Numbering**
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ **Non-ASCII**
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ **Variable Length**
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ **PatentIn ver. 2.0 "bug"**
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.**

8 _____ **Skipped Sequences (OLD RULES)**
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ **Skipped Sequences (NEW RULES)**
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ **Use of n's or Xaa's (NEW RULES)**
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ **Use of <213>Organism (NEW RULES)**
Sequence(s) _____ are missing this mandatory field or its response.

12 _____ **Use of <220>Feature (NEW RULES)**
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ **PatentIn ver. 2.0 "bug"**
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

1647

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/267,963B*

DATE: 04/02/2001
TIME: 22:24:55

INPUT SET: S36584.raw

> This Raw Listing contains the General
> Information Section and those Sequences
> containing ERRORS.

pp 2, 4-5

SEQUENCE LISTING

Does Not Comply
Corrected Diskette Needed

```
 1                              SEQUENCE LISTING
 2
 3   (1)     General Information:
 4
 5       (i) APPLICANT:  Kohei MIYAZONO; Takeshe IMAMURA; Peter DEN DIJKE
 6
 7      (ii) TITLE OF INVENTION:   ISOLATED ALK-1 PROTEIN, NUCLEIC ACIDS ENCODING
 8           IT, AND USES THEREOF
 9
10     (iii) NUMBER OF SEQUENCES: 46
11
12      (iv) CORRESPONDENCE ADDRESS:
13           (A) ADDRESSEE:  Fulbright & Jaworski L.L.P.
14           (B) STREET:     666 Fifth Avenue
15           (C) CITY:       New York City
16           (D) STATE:      New York
17           (E) COUNTRY:    USA
18           (F) ZIP:        10103
19
20       (v) COMPUTER READABLE FORM:
21           (A) MEDIUM TYPE:  Diskette, 3.25 inch, 1.44mb
22           (B) COMPUTER:  IBM PS/2
23           (C) OPERATING SYSTEM:  PC-DOS
24           (D) SOFTWARE:  Wordperfect
25
26      (vi) CURRENT APPLICATION DATA:
27           (A) APPLICATION NUMBER: 09/267,963
28           (B) FILING DATE: March 12, 1999
29           (C) CLASSIFICATION: 435
30
31     (vii) PRIOR APPLICATION DATA:
32           (A) APPLICATION NUMBER: PCT/GB93/02367
33           (B) FILING DATE: November 17, 1993
34
35     (vii) PRIOR APPLICATION DATA:
36           (A) APPLICATION NUMBER: GB 9224057.1
37           (B) FILING DATE: November 17, 1992
38
39     (vii) PRIOR APPLICATION DATA:
40           (A) APPLICATION NUMBER: GB 9304677.9
41           (B) FILING DATE: March 8, 1993
42
43     (vii) PRIOR APPLICATION DATA:
44           (A) APPLICATION NUMBER: GB 9304680.3
45           (B) FILING DATE: March 8, 1993
```

--> (line 29)

INPUT SET: S36584.raw

```
46
47        (vii) PRIOR APPLICATION DATA:
48              (A) APPLICATION NUMBER: 9311047.6
49              (B) FILING DATE: May 28, 1993
50
51        (vii) PRIOR APPLICATION DATA:
52              (A) APPLICATION NUMBER: 9313763.6
53              (B) FILING DATE: July 2, 1993
54
55        (vii) PRIOR APPLICATION DATA:
56              (A) APPLICATION NUMBER: 9136099.2
57              (B) FILING DATE: August 3, 1993
58
59        (vii) PRIOR APPLICATION DATA:
60              (A) APPLICATION NUMBER: 321344.5
61              (B) FILING DATE: October 15, 1993
62
63        (vii) PRIOR APPLICATION DATA:
64              (A) APPLICATION NUMBER: 09/039,177
65              (B) FILING DATE: March 13, 1998
66
67       (viii) ATTORNEY/AGENT INFORMATION:
68              (A) NAME: Mary Anne Schofield
69              (B) REGISTRATION NUMBER: 36,669
70              (C) REFERENCE/DOCKET NUMBER: LUD 5539.1 CIP - JEL/MAS
71
72         (ix) TELECOMMUNICATION INFORMATION:
73              (A) TELEPHONE: (212) 318-3000
74              (B) TELEFAX:   (212) 318-3400
75
76
```

ERRORED SEQUENCES FOLLOW:

```
2716    (2) INFORMATION FOR SEQ ID NO: 34:
2717        (i) SEQUENCE CHARACTERISTICS:
2718            (A) LENGTH: 513 amino acids
-->  2719       (B) TYPE: amino acid
2720            (D) TOPOLOGY: linear
2721
2722    (ii) MOLECULE TYPE: peptide
2723
2724    (vi) ORIGINAL SOURCE:
2725         (A) ORGANISM: MOUSE
2726
2727    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:
2728
2729 Met Gly Ala Ala Ala Lys Leu Ala Phe Ala Val Phe Leu Ile Ser Cys
2730                  5                   10                  15
2731 Ser Ser Gly Ala Ile Leu Gly Arg Ser Glu Thr Gln Glu Cys Leu Phe
```

> delete "7"

RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/267,963B*

INPUT SET: S36584.raw

```
2732                    20                   25                   30
2733      Phe Asn Ala Asn Trp Glu lys Asp Arg Thr Asn Gln Thr Gly Val Glu
2734              35                   40                   45
2735      Pro Cys Tyr Gly Asp Lys Asp Lys Arg Arg His Cys Phe Ala Thr Trp
2736          50                   55                   60
2737      Lys Asn Ile Ser Gly Ser Ile Glu Ile Val Lys Gln Gly Cys Trp Leu
2738      65                   70                   75                   80
2739      Asp Asp Ile Asn Cys Tyr Asp Arg Thr Asp Cys Val Glu Lys Lys Asp
2740                  85                   90                   95
2741      Ser Pro Glu Val Tyr Phe Cys Cys Cys Glu Gly Asn Met Cys Asn Glu
2742              100                  105                  110
2743      Lys Phe Ser Tyr Phe Pro Glu Met Glu Val Thr Gln Pro Thr Ser Asn
2744              115                  120                  125
2745      Pro Val Thr Pro Lys Pro Pro Tyr Tyr Asn Ile Leu Leu Tyr Ser Leu
2746          130                  135                  140
2747      Val Pro Leu Met Leu Ile Ala Gly Ile Val Ile Cys Ala Phe Trp Val
2748      145                  150                  155                  160
2749      Tyr Arg His His Lys Met Ala Tyr Pro Pro Val Leu Val Pro Thr Gln
2750                  165                  170                  175
2751      Asp Pro Gly Pro Pro Pro Pro Ser Pro Leu Leu Gly Leu Lys Pro Leu
2752              180                  185                  190
2753      Gln Leu Leu Glu Val Lys Ala Arg Gly Arg Phe Gly Cys Val Trp Lys
2754              195                  200                  205
2755      Ala Gln Leu Leu Asn Glu Tyr Val Ala Val Lys Ile Phe Pro Ile Gln
2756          210                  215                  220
2757      Asp Lys Gln Ser Trp Gln Asn Glu Tyr Glu Val Tyr Ser Leu Pro Gly
2758      225                  230                  235                  240
2759      Met Lys His Glu Asn Ile Leu Gln Phe Ile Gly Ala Glu Lys Arg Gly
2760                  245                  250                  255
2761      Thr Ser Val Asp Val Asp Leu Trp Leu Ile Thr Ala Phe His Glu Lys
2762                  260                  265                  270
2763
2764      Gly Ser Leu Ser Asp Phe Leu Lys Ala Asn Val Val Ser Trp Asn Glu
2765              275                  280                  285
2766      Leu Cys His Ile Ala Glu Thr Met Ala Arg Gly Leu Ala Tyr Leu His
2767          290                  295                  300
2768      Glu Asp Ile Pro Gly Leu Lys Asp Gly His Lys Pro Ala Ile Ser His
2769      305                  310                  315                  320
2770      Arg Asp Ile Lys Ser Lys Asn Val Leu Leu Lys Asn Asn Leu Thr Ala
2771                  325                  330                  335
2772      Cys Ile Ala Asp Phe Gly Leu Ala Leu Lys Phe Glu Ala Gly Lys Ser
2773              340                  345                  350
2774      Ala Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr Met Ala Pro
2775              355                  360                  365
2776      Glu Val Leu Glu Gly Ala Ile Asn Phe Gln Arg Asp Ala Phe Leu Arg
2777          370                  375                  380
2778      Ile Asp Met Tyr Ala Met Gly Leu Val Leu Trp Glu Leu Ala Ser Arg
2779      385                  390                  395                  400
2780      Cys Thr Ala Ala Asp Gly Pro Val Asp Glu Tyr Met Leu Pro Phe Glu
2781              405                  410                  415
2782      Glu Glu Ile Gly Gln His Pro Ser Leu Glu Asp Met Gln Glu Val Val
2783              420                  425                  430
2784      Val His Lys Lys Lys Arg Pro Val Leu Arg Asp Tyr Trp Gln Lys His
```

INPUT SET: S36584.raw

```
2785            435               440               445
2786    Ala Gly Met Ala Met Leu Cys Glu Thr Ile Glu Glu Cys Trp Asp His
2787            450               455               460
2788    Asp Ala Glu Ala Arg Leu Ser Ala Gly Cys Val Gly Glu Arg Ile Thr
2789    465               470               475               480
2790    Gln Met Gln Arg Leu Thr Asn Ile Ile Thr Thr Glu Asp Ile Val Thr
2791            485               490               495
2792    Val Val Thr Met Val Thr Asn Val Asp Phe Pro Pro Lys Glu Ser Ser
2793            500               505               510
2794    Leu
2795
2796
```

```
2967    (2)  INFORMATION FOR SEQ ID NO: 37:
2968         (i)  SEQUENCE CHARACTERISTICS:          → 97 shown)
-->  2969         (A) LENGTH: 102 amino acids
-->  2970         (B) TYPE: amino acid              → delete "?"
2971         (D) TOPOLOGY: linear
2972
2973    (ii) MOLECULE TYPE: peptide
2974
2975    (vi) ORIGINAL SOURCE:                    misaligned amino
2976         (A) ORGANISM: C. elegans            acid nos. (see item 4
2977                                              on Error
2978    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:  summary
2979                                              sheet)
2980    Cys His Cys Ser Arg Glu Val Gly Cys Asn Ala Arg Thr Thr Gly Trp
2981                                                    5               10
2982    Val Pro Gly Ile Glu Phe Leu Asn Glu Thr Asp Arg Ser Phe Tyr Glu
2983                                  20              25              30
2984    Asn Thr Cys Tyr Thr Asp Gly Ser Cys Tyr Gln Ser Ala Arg Pro Ser
2985                                          35              40
2986    Pro Glu Ile Ser His Phe Gly Cys Met Asp Glu Lys Ser Val Thr Asp
2987                                      50              55              60
2988    Glu Thr Glu Phe His Asp Thr Ala Ala Lys Val Cys Thr Asn Asn Thr
2989                                          65              70
2990    Lys Asp Pro His Ala Thr Val Trp Ile Cys Cys Asp Lys Gly Asn Phe
2991                                              85              90
2992    Cys
2993
2994
2995
2996
2997
```

```
3121    (2)  INFORMATION FOR SEQ ID NO:46:
3122         (i)  SEQUENCE CHARACTERISTICS:    ← mandatory response needed (6 shown
-->  3123         (A) LENGTH:? amino acids                              on nxt
3124         (B) TYPE: amino acid                                      page)
3125         (D) TOPOLOGY: linear
3126
3127    (ii) MOLECULE TYPE: peptide
3128
```

RAW SEQUENCE LISTING
PATENT APPLICATION   US/09/267,963B

INPUT SET: S36584.raw

```
3129      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:
3130
3131    Gly Thr Ala Arg Tyr Met
3132                        5 S
3133
```

misaligned number

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/09/267,963B*

INPUT SET: S36584.raw

Line	Error	Original Text
29	Wrong Classification	(C) CLASSIFICATION: 435
2719	Unknown or Misplaced Identifier	(B) TY7PE: amino acid
2969	Entered (102) and Calc. Seq. Length (97) differ	(A) LENGTH: 102 amino acids
2970	Unknown or Misplaced Identifier	(B) TY7PE: amino acid
3123	Length must be an Integer	(A) LENGTH: amino acids
3123	Entered (0) and Calc. Seq. Length (6) differ	(A) LENGTH: amino acids